

GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: June 1, 2003, 15:21:24 ; Search time 2812.92 Seconds
(without alignments)
12850.800 Million cell updates/sec

Title: US-09-625-573-1
Perfect score: 2232
Sequence: 1 GGATTGAACAGGACGCATT.....TATAACTATGTTGATAAAG 2232

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1:	em_estba:*
2:	em_esthum:*
3:	em_estin:*
4:	em_estmu:*
5:	em_estov:*
6:	em_estpl:*
7:	em_estro:*
8:	em_htc:*
9:	gb_est1:*
10:	gb_est2:*
11:	gb_htc:*
12:	gb_est3:*
13:	gb_est4:*
14:	gb_est5:*
15:	em_estfun:*
16:	em_estom:*
17:	gb_gss:*
18:	em_gss_hum:*
19:	em_gss_inv:*
20:	em_gss_pin:*
21:	em_gss_vrt:*
22:	em_gss_fun:*
23:	em_gss_mam:*
24:	em_gss_mus:*
25:	em_gss_other:*
26:	em_gss_pro:*
27:	em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	459.8	21.0	807	13	BI764263
2	456.6	20.5	469	10	AV715904
3	442.8	19.8	457	9	AA694175
4	421.4	18.9	563	9	AA034153
5	394.8	17.7	398	9	AA807940
6	390.2	17.5	407	14	BQ027284

c	7	360	16.1	467	14	H58254
c	8	357.6	16.0	487	10	BB656336
	9	346.8	15.5	461	14	H58245
	10	326.2	14.6	542	9	AA547303
	11	302	13.5	410	14	H58584
	12	296.4	13.3	480	10	AA657263
	13	293.4	13.1	422	14	H58597
	14	292.6	13.1	447	9	AA671573
	15	289	12.9	1074	14	BM917063
c	16	268.2	12.0	289	9	AA034154
	17	266.6	11.9	907	9	AL552677
	18	249.8	11.2	789	12	BG205056
	19	236.4	10.6	876	13	BI908283
	20	235.2	10.5	884	12	BG182330
	21	220.8	9.9	952	14	BM917763
	22	216.8	9.7	745	12	BG204024
c	23	214.6	9.6	1167	14	BQ053936
	24	212.8	9.5	452	9	AI851510
	25	197	8.8	672	10	BB638766
	26	189	8.5	780	13	BI908127
	27	188.4	8.4	568	12	BF193051
	28	186.8	8.4	551	12	BF081124
	29	181	8.1	863	13	BF661279
	30	180.6	8.1	669	13	BI393893
	31	179.4	8.0	533	12	BF193021
	32	177.2	7.9	639	10	BB629533
	33	175.2	7.8	723	14	BM951933
	34	173.6	7.8	965	14	BQ944555
	35	172.2	7.7	934	12	BG460984
	36	171	7.7	207	12	BG315432
	37	169.2	7.6	787	9	AU080004
	38	164.4	7.4	3005	11	AK019478
	39	163.8	7.3	936	12	BF119806
	40	153.2	6.9	665	10	BB628567
	41	151.8	6.8	662	10	BB644135
	42	151.6	6.8	600	13	BI987229
	43	151.6	6.8	646	10	BB615654
	44	147.4	6.6	869	12	BF119225
	45	147.2	6.6	867	13	BI106339

ALIGNMENTS

RESULT 1
BI764263
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES

BI764263 807 bp mRNA linear EST 25-SEP-2001
603045953F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5186388 5',
mRNA sequence.
BI764263
BI764263.1 GI:15755841
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 807)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11465 row: i column: 13
High quality sequence stop: 805.
Location/Qualifiers
1. .807

H58254 YR06H06.s1
BB656336 UI-M-BH0-
H58245 YR06F06.s1
AA547303 YK28H04.r
H58584 YR06F06.r1
AA657263 109996 MA
H58597 YR06H06.r1
AA671573 V104G01.r
BM917063 AGENCOURT
AA034154 Z106F10.s
AL552677 AL552677
BG205056 RST24475
BI908283 603063222
BG182330 RST1196 A
BM917763 AGENCOURT
BG204024 RST23417
BQ053936 AGENCOURT
AI851510 UI-M-BH0-
BB638766 BB638766
BI908127 603067423
BF193051 244485 MA
BF081124 233997 MA
BF661279 603304243
BI393893 P9P1n.pk0
BF193021 244450 MA
BB629533 BB629533
BM951933 UI-M-EH0-
BQ944555 AGENCOURT
BG460984 RST43688
BG315432 P02.0.308
AU080004 AU080004
AK019478 Mus muscu
BF119806 601758673
BB628567 BB628567
BB644135 BB644135
BI987229 3193-25 M
BB615654 BB615654
BF119225 601737232
BI106339 602890674

Db 385 CCTATGGTAAAGTAAGTGGAGAGGCTCCTCGAAGTAAGCAAAAGACTTTCCTC 326

QY 1916 TTATGTCGAG-CCAAGTTAAGAAATGTTCTTATGTTGCCAGTGTGTTCTGATCTGATGCA 1974

Db 325 TTATGTCGAGCCCAAGTAAAGATGTTCTTATGTTGCCAGTGTGTTCTGATCTGATGCA 266

QY 1975 ACAGAAACACTGGCTTCTAGAA-CCAGCAACTTGGGAACCTAGACTCCCAAGCTGGA 2033

Db 265 AGCAAGAAACACTGGCTTCTAGAAACCAGCAACTTGGGAACCTAGACTCCCAAGCTGGA 206

QY 2034 CTATGGCTCTACTTTCAGGCCACATGCTAAAGAGGTTTCAGAAAGAGTGGGGACAGA 2093

Db 205 CTATGGCTCTACTTTCAGGCCACATGCTAAAGAGGTTTCAGAAAGAGTGGGGACAGA 146

QY 2094 GCAGAACTTTCACCTTCATATATTTGATGATCCTTAATGAAATGATGATGATGATGATG 2153

Db 145 GCAGAACTTTCACCTTCATATATTTGATGATCCTTAATGAAATGATGATGATGATGATG 86

QY 2154 ATGCTGATGAATCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2213

Db 85 ATGCTGATGAATCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 26

QY 2214 ATAACTATGTTGATAAAA 2231

Db 25 ATAACTATGTTGATAAAA 8

RESULT 8

BE656336

LOCUS

DEFINITION

UI-M-BHO-aju-h-06-0-UI.r1 NIH_BMAP_M.S1 Mus musculus CDNA clone

UI-M-BHO-aju-h-06-0-UI 5', mRNA sequence.

ACCESSION

BE656336

VERSION

1

KEYWORDS

EST.

SOURCE

house mouse.

ORGANISM

Mus musculus

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS

Bonaldo, M.F., Lennon, G. and Soares, M.B.

TITLE

Normalization and subtraction: two approaches to facilitate gene discovery

JOURNAL

Genome Res. 6 (9), 791-806 (1996)

MEDLINE

9704477

COMMENT

Contact: Chin, H

National Institute of Mental Health

6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD

20892-9643, USA

Tel: 301 443 1706

Fax: 301 443 9890

Email: mEST@mail.nih.gov

CDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP CDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements

Seq primer: M13 Reverse.

FEATURES

source

1. 487

Location/Qualifiers

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UI-M-BHO-aju-h-06-0-UI"

/clone_lib="NIH_BMAP_M.S1"

/dev_stage="27-32 days"

/lab_host="DH10B (Life Technologies)"

/notes="vector: pRT3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The NIH_BMAP_M.S1 library is a subtracted library derived from a mixture of normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs,

hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus). The driver used for subtraction consisted of a pool of 20,000 cDNA clones obtained from non-normalized and normalized libraries of these ten regions of the mouse brain."

BASE COUNT 115 a 115 c 103 g 154 t

Query Match 16.0%; Score 357.6; DB 10; Length 487;
Best Local Similarity 85.3%; Pred. No. 8.9e-82;
Matches 399; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 110 TTGATTATGATTACGGTCTCCCTGTCTATAAATTTGACGTGAAGCAAAATTTGGGGCCCAAC 169

Db 19 TCGATTATGTTATGTCAGCACCCCTGCCAAAAAATCAATGTGAACAAATTTGGGCTCAGC 78

QY 170 TCCTGCCCTCCGCTCTACTCGCTGTGTTTCATCTTTGTTTGGTGGTGGCAACATGCTGGTGG 229

Db 79 TCCTGCCCTCCGCTCTACTCGCTGTGTTTCATCTTTGTTTGGTGGTGGCAACATGATGGTCT 138

QY 230 TCCTCATCTTAAATAAAGCTGCAAAAGCTGAAGTCTTTCACGTGACATTTTACCTGCTCAACC 289

Db 139 TCCTCATCTTAAATAAAGCTGCAAAAGCTGAAGTCTTTCACGTGACATTTTACCTGCTCAACC 198

QY 290 TGGCCATCTCTGATCTGCTTTTCTTATTTACTCTCCCATTTGGGGTCACTCTGCTGCA 349

Db 199 TGGCCATCTCTGATCTGCTTTTCTTATTTACTCTCCCATTTGGGGTCACTCTGCTGCA 258

QY 350 ATGAGTGGTCTTTGGGAATGCAATGTGCAAAATTTTACAGGGCTCTATCACATCGT 409

Db 259 ATGAGTGGTCTTTGGGAATGCAATGTGCAAAATTTTACAGGGCTCTATCACATCGT 318

QY 410 ATTTTGGGGAAATCTTCTTTCATCATCTCTCTGCAATGATAGATGCTGGTATGTC 469

Db 319 ATTTTGGGGAAATCTTCTTTCATCATCTCTCTGCAATGATAGATGCTGGTATGTC 378

QY 470 ATGCTGTGTTTCTTAAAGCCAGGCGTCACTTTCGGGGTGCACAGTGTGATCA 529

Db 379 ATGCTGTGTTTCTTAAAGCCAGGCGTCACTTTCGGGGTGCACAGTGTGATCA 438

QY 530 CTGTTGGTGGTCTGTTTGGTCTCTGCTCCAGGAATCATCTTTACTA 577

Db 439 CTGTTGGTGGTCTGTTTGGTCTCTGCTCCAGGAATCATCTTTACTA 486

H58245 461 bp mRNA linear EST 05-OCT-1995

Y:06f06.s1 Soares fetal liver spleen lNELS Homo sapiens CDNA clone

IMAGE:204515 3', mRNA sequence.

H58245

ACCESSION

VERSION

1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 461)

AUTHORS

Hillier, L., Clark, N., Dubouque, T., Elliston, K., Hawkins, M., Holman, R., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisan, E., Waterston, R., Williamson, A., Wohlmann, P., and Wilson, R.

TITLE

The WashU-Merck EST Project.

JOURNAL

Unpublished (1995)

COMMENT

Contact: Willson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 1007

High quality sequence stops: 335

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1007 Std Error: 0.00

FEATURES

I. 461

```
/organism="Homo sapiens"
/db_xref="GDB:3773646"
/db_xref="taxon:9606"
/clone="IMAGE:204515"
/clone_lib="Soares fetal liver spleen lNFLS"
/sex="male"
/dev_stage="20 week post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/notes="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;
1st strand cDNA was primed with _Pac I - oligo(dT) primer
[5' AACTGGAGGAATTAATTAAGACATCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Patima Bonaldo."
```

97.6 96.6 144 t
5 others

BASE COUNT	119 a	97 c	96 g	144 t	5 others
ORIGIN					
Query Match		15.5%	Score 346.8;	DB 14;	Length 461;
Best Local Similarity		92.6%;	Pred. No. 5.6e-79;		
Matches 427: Conservative		0: Mismatches 27;	Indels 7;	Gaps 6;	

QY	1776	ATGTCCTTGATGCATCATATTGTTCCTTAATTTGCCAGTGGGAACCTCCTAATCAAAATGG	1835
Db	461	ANGGCCCTGAGCCCAAATGNCOCCTTANTTGCOCAGNGGAAACCCCTAAACCAGATGG	402
QY	1836	CTT-CTAATCAAGACTTTTTAAA-CCCTATTGGTAAAGAATGGAAGTGGAGAAGCT-CCC	1892
Db	401	CCTCCTAATCAAGAGCTTTTTAAACCCCTATTGGTAAAGATGGAGGTGGAGAAGCTCCCC	342
QY	1893	TGAAGTAG-CAAGAGACTTTCTCTTAGTCGAGCCAAAGTTAAGAATGTTCTTATGTTG-	1949
Db	341	TGAAGTAGGCAAGAGACTTTCCCCCTTAGTCGAGCCAAGTTAAGAATGTTCTTATGTTGC	282
QY	1950	CCGAGTGTGTTCTGATCTGATGCAAGCAAGAACACACTGGGCTTCTAGAA-CCAGGCAAC	2008
Db	281	CCCAGTGTGTTCTGATCTGATGAAGCAAGCAAGACCTGGGCTTCTAGACCAGGCAAC	222
QY	2009	TTGGGACTAGACATCCCAAGCTGGACTATGCTCTACTTTTCAGGCCACATGGCTAAAGAA	2068
Db	221	TTGGGACTAGACTCCCAAGCTGGACTATGCTCTACTTTTCAGGCCACATGGCTAAAGAA	162
QY	2069	GGTTTCAGAAAGAGTGGGGACAGACAGAACTTTCACCTTCATATATTTGTATGATCCT	2128
Db	161	GGTTTCAGAAAGAGTGGGGACAGACAGAACTTTTCACCTTCATATATTTGTATGATCCT	102
QY	2129	AATGAATGCATAAAATGTTTAAGTTCATGGTGATGAAATGTAATACTGTGTTTTTACAAC	2188
Db	101	AATGAATGCATAAAATGTTAAGTTCATGGTGATGAAATGTAATACTGTGTTTTTACAAC	42
QY	2189	ATGATTTGGAAAAATAAATCAATGCCTATTAACATATGTTGTATAA	2229
Db	41	ATGATTTGGAAAAATAAATCAATGCCTATTAACATATGTTGTATAA	1

RESULT 10	AA547303	542 bp	linear	EST 05-AUG-1997
LOCUS	AA547303			
DEFINITION	IMAGE:047959 5' similar to SW:KRR2.HUMAN P41597 MONOCYTE CHEMOATTRACTANT PROTEIN 1 RECEPTOR ;, mRNA sequence.			
ACCESSION	AA547303			
VERSION	AA547303.1	GI:2308594		
KEYWORDS	EST.			

SOURCE
ORGANISM

house mouse.
Mus musculus

ORGANISM	Mus musculus
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 542)

REFERENCE
AUTHORS

TITLE	JOURNAL	COMMENT
1. The Role of the Teacher in the Classroom	Journal of Educational Research	1965, Vol. 68, No. 1, pp. 1-10
2. The Impact of Technology on Education	Journal of Educational Technology	1970, Vol. 1, No. 2, pp. 1-10
3. The Importance of Parental Involvement	Journal of Educational Psychology	1975, Vol. 66, No. 3, pp. 1-10
4. The Effect of Teacher Expectations on Student Achievement	Journal of Educational Research	1980, Vol. 83, No. 4, pp. 1-10
5. The Role of the School in the Community	Journal of Educational Research	1985, Vol. 88, No. 5, pp. 1-10
6. The Impact of Teacher Education on Student Achievement	Journal of Educational Research	1990, Vol. 93, No. 6, pp. 1-10
7. The Role of the Teacher in the Classroom	Journal of Educational Research	1995, Vol. 98, No. 7, pp. 1-10
8. The Impact of Technology on Education	Journal of Educational Technology	2000, Vol. 11, No. 8, pp. 1-10
9. The Importance of Parental Involvement	Journal of Educational Psychology	2005, Vol. 96, No. 9, pp. 1-10
10. The Effect of Teacher Expectations on Student Achievement	Journal of Educational Research	2010, Vol. 113, No. 10, pp. 1-10
11. The Role of the School in the Community	Journal of Educational Research	2015, Vol. 118, No. 11, pp. 1-10
12. The Impact of Teacher Education on Student Achievement	Journal of Educational Research	2020, Vol. 123, No. 12, pp. 1-10

TITLE The WashU-HHMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Marra M/Mouse EST Project
 WashU-HHMI Mouse EST Project
 Washington University School of Medicine
 660 South Euclid Avenue
 St. Louis, MO 63108

Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact
IMAGE Consortium (info@image.llnl.gov) for further info.
MGI: 544815

FEATURES

```

i. .342
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_name="IMAGE:947959"
/clone_lib="Soares_mammary_gland_NBMMG"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/note="Organ: mammary gland; Vector: pTET
RI; 1st strand cDNA was primed with a N
primer [5'
TGTTACCAATCTCAATGGGAGCGCCGATGGTTT
T 3']; double-stranded cDNA was ligated
adaptors (Pharmacia), digested with Not
the Not I and Eco RI sites of the modifi
RNA provided by Dr. Minoru Ko, Wayne Soes
constructed and normalized by Bento Soes
Bonaldo."

```

	131 a	126 c	113 g	172 t
BASE COUNT				
ORIGIN				

Query Match	14.6%;	Score 326.2;	DB 9;	Length 542;
Best Local Similarity	79.2%;	Pred. No. 1.3e-73;		
Matches 430;	Conservative	0;	Mismatches 98;	Indels 15

383	QY	TATTCACAGGGCTGTATCATCATCGGTTATTTGGCGGAATCTTCTTCATCATCCCTCTCA	442
		3 TATTCACAGGGCTCTATCATCATTTGGTTATTTTGGTGGAAATCTTCTTCATTAATCTCTCTCA	62
443	QY	CAATCATAGATACCTGGCTATTGTCCATGCTCTGTTTGGCTTTAAAGCCAGACAGGTCA	502
		63 CAATTGATAGGTACTTGGCTATTGTCCATGCTCTGTTTGGCTTTAAAGTCAGAAAGGTCA	122
503	QY	CCTTTGGGGTGTGACAAGTGTGATCATCCTGGTTGGTGGCTGTTGGCTCTGTCTCCACAG	562
		123 ACTTTGGGGTGATAACAAGTGTAGTCACTTTGGGCGGTGGCTGTTGGCTCTCTCTCCAG	182
563	QY	GAATCATCTTTACTTAATGCCAGAAAGATTCGTGTTTATGCTCTGGGCGCTTATTTTC	622
		183 AATAATCTTTACCATGATCTCAGAAAGGTTTTCATTATACATGCAGTCCCTCATTTTC	242
623	QY	CA-----CGAGGATGGAAATTTTCCACACAATAATGAGGAACATTTTGGGGC	670
		243 CACACACTCAGTATCATTTCTTGGAGAGTTTCCAAACATTAAGATGGTCATCTTGAGCC	302
671	QY	TGGTCTCCGCGCTGCTCATCATGTCATCTCGGGAACCTCGAAACCCCTGCTTC	730

Mon Jun 2 09:42:08 2003

QY 280 CTGCTACACCTGGCCATCTGATCTGCTTTTCTTATTAATCTCCCAATCTGGGCTCAC 339
 Db 243 CTCCTGAACCTGGCCATCTGATCTGCTTTTCTTATTAATCTCCCAATCTGGGCTCAC 302
 QY 340 TCTGCTGCAA---ATGAGTGGGTCTTTGGGAATGCAATGTGCAAAATATTACAGGGCTG 396
 Db 303 TACAACTTGAAGGATGACTGGGTCTTTGGTGTATGATGCTGTAAGATCTCTCTGGGTTT 362
 QY 397 TATCACATCGGTATTTTGGGGGATCTCTTCATCATCTCCCTCTGACAAATCGATAGATAC 456
 Db 363 TATTACACAGGCTTTACAGGAGATCTTTTCATCATCTCCCTCTGACGAATGACAGGTAC 422
 QY 457 CTGGCTATTGTCCATGCTGTGTTGCTTTAAAGCCAGCAGCGTCACTTTGGGGTGGTG 516
 Db 423 CTGGCCATCGTCCACGCGGTGTTGGCTTGGGGGACGACCGCTCACTTTGGGTGTATC 482
 QY 517 ACAAGTGTGATCACCTGGTGGTGGTGTGTTGCTTCTGTCCTCCAGGAATCATCTTACT 576
 Db 483 ACCAGCATCATCATTTGGGCCCTGGCCATCTTTGGCTTCCATGCCAGGCTTATACTTTCC 542
 QY 577 AATGCCAGAAAGAGATTCTGTTATGCTGTGGCCCTTATTTTCC-----A 624
 Db 543 AAGACCAATGGGAATTCATCACACACCTGCAGCCTTCACTTTCTCACGAAAGCCTA 602
 QY 625 CGAGGATGGAATAATTTCCACACAATAATGAGAAACATTTGGGGCTGGTCTGCGGCTG 684
 Db 603 CGAGAGTGGAAAGTGTTCAGGCTCTGAAACTGAACCTCTTTGGGGTGGTATTCGCTTTG 662
 QY 685 CTATCATGTCATCTGCTACTCGGGAATCCTGAAACCTGCTTCGGTGTGAAACGAG 744
 Db 663 TTGGTCATGATCATCTGCTACACAGGATTAAGATTTCTGCTAAGACGACCAATGAG 722
 QY 745 AAGAAGAGGCATAGGGCAGTGAGATCATCTTCACCATCATGATTTTACTTTCTCTTC 804
 Db 723 AAGAA---ATCCAAAGCTGTCCTGATTTTGTATCATCATGATCATCTTTTCTCTTT 779
 QY 805 TGGACTCCCTATAACATTTGCTATCTCTGACACACCTTCAGGAATTTCTGCGCTGAGT 864
 Db 780 TGGACCCCTTACNATTGATATATCTGTTTCTGTTTCCAGACITTCCTGTTACCCAT 839
 QY 865 AACTGTGAAGCAGCAGTCAACTGAGCAAGCCAGCAGGCTGACAGAGACTCTTGG 920
 Db 840 GAGTGTGAGCAGCAGACATTTGGACCTGGCTGTGCAAGTGAACGGAAGTATCG 895

Search completed: June 1, 2003, 20:03:35
 Job time : 2826.92 secs

